REMARKS

New Tables 4 and 5 are provided to substitute for original Tables 4 and 5 found at pages

68-76. The Substitute Tables 4 and 5 provide reference to the SEQ ID Nos. found in the

Sequence Listing. A set of marked-up Tables 4 and 5 is also provided with highlighting to show

the changes from the original Tables 4 and 5. No new matter has been entered.

A Sequence Listing paper copy is also provided for insertion into the Specification.

It is believed that no additional fee is due; however, should any additional fees under 37

C.F.R. §§ 1.16 to 1.21 be required for any reason relating to the enclosed materials, the

Commissioner is authorized to deduct said fees from Deposit Account No. 01-

2508/**11362.0038.NPUS01**.

The Examiner is invited to contact the undersigned attorney at (713) 787-1438 with any

questions, comments or suggestions relating to the referenced patent application.

Respectfully submitted,

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713 787 1400

Date: October 27, 2003

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Table 4. Differential expression of Apo E isoforms in AD patients versus contrast groups.

Apo E	Iq	MW	6 AD vs.	6 AD	6 AD vs.	6 AD vs.	Aa#	Peptide sequence #	Seq ID
NPI		(kDa)	Q 9	vs. 6 FTD	10 FTD	4 VAD	start-end		No.
34	5.11	35.2	 →	11	11	11	270-278	LQAEAFQAR	-
		-					259-269	AKLEEQAQQIR	7
							166-175	LLRDADDLQK	3
٠							19-33	KVEQAVETEPEPELR	4
35	5.32	34.3	\rightarrow	pu	pu	pu	270-278	LQAEAFQAR	
							259-269	AKLEEQAQQIR	7
							199-207	LGPLVEQGR	5
							301-317 (C-term.)	VQAAVGTSAAPVPSDNH	9
72	2.07	15.8]]	11	pu	pu	199-207	LGPLVEQGR	2
							270-278	LQAEAFQAR	_
							259-269	AKLEEQAQQIR	7
73	5.11	15.8	11	II	11	II	270-278	LQAEAFQAR	_
74	4.91	15.8	II	11	II	\rightarrow	199-207	LGPLVEQGR	2
							270-278	LQAEAFQAR	_
							259-269	AKLEEQAQQIR	2
							210-224	AATVGSLAGQPLQER	7
							138-152	GEVQAMLGQSTEELR	∞
							94-108	SELEEQLTPVAEETR	6
							301-317 (C-term.)	VQAAVGTSAAPVPSDNH	9
75	5.09	15.1	H	pu	pu	pu	138-152	GEVQAMLGQSTEELR	∞
							19-33	KVEQAVETEPEPELR	4
							270-278	LQAEAFQAR	_
41	2.07	15.3	\rightarrow	pu	pu	pu	19-33	KVEQAVETEPEPELR	4
							270-278	LQAEAFQAR	_
9/	5.24	13.8	→	→	II	\rightarrow	210-224	AATVGSLAGQPLQER	7
11	4.96	12.4	()=	II	II	11	259-269	AKLEEQAQQIR	7
52	5.30	33.8	→	pu	pu	pu	270-278	LQAEAFQAR	

Table 4. Differential expression of Apo E isoforms in AD patients versus contrast groups.

Apo E	pI	MW	6 AD vs.	6 AD	6 AD vs.	6 AD vs.	Aa#	Peptide sequence #	Seq ID
Ida		(kDa)	Q 9	vs. 6 FTD	10 FTD	4 VAD	start-end		No.
							199-207	LGPLVEQGR	5
							259-269	AKLEEQAQQIR	7
							06-08	ALMDETMKELK	10
09	5.38	15.6	\rightarrow	ы	pu	pu	19-33	KVEQAVETEPEPELR	4
99	5.17	30.	↑ or	pu	pu	pu	199-207	LGPLVEQGR	5
			1				61-16	AYKSELEEQLTPVAEETR	11
							111-121	LSKELQAAQAR	12
							210-224	AATVGSLAGQPLQER	7
							259-269	AKLEEQAQQIR	2
							270-278	LQAEAFQAR	
=	5.22	35.3	pu	70↑	pu	pu	19-33	KVEQAVETEPEPELR	4
							91-109	AYKSELEEQLTPVAEETR	11
							111-121	LSKELQAAQAR	12
							210-224	AATVGSLAGQPLQER	7
							259-269	AKLEEQAQQIR	2
							270-278	LQAEAFQAR	
Only group	itativa racii	to ore chouse	od fwith the	voontion	NDI 66 and N	IDI 11 mhoro	tip outitotilano dit	Only anontitative recults are choused (with the evecantion of NIDI of and NIDI 11 whose only a anolitative difference (OI) und formal	

Only quantitative results are showed (with the exception of NPI 66 and NPI 11, where only a qualitative difference (QL) was found). \forall : down-regulated in AD $\{ \psi : p < 0.05; = (\psi) : p < 0.07 \}$ =: upregulated in AD $\{ \uparrow : p < 0.05; = (\uparrow) : p < 0.07 \}$ =: no significant difference #: peptide sequences covered by MS analysis and: not detected

Table 5. Identification of the protein spots that were altered between the studied groups.

Spot	Spot	Peptide	Seq ID No.	aa	Identification in database	ID number
exp1	exp2					database
2713	674	TDTSHHDQDHPTFNK	. 13	35-49	Alpha-1-antitrypsin	P01009
		LVDKFLEDVK	14	150-159		
		FLEDVKK	15	154-160		
		KQINDYVEK	16	179-187		
		QINDYVEK	17	180-187		
		DTEEEDFHVDQATTVK (M1A allele)	18	226-241	•	
		DTEEEDFHVDQVTTVK (M1V allele)	61	226-241		
		LQHLENELTHDIITK	20	284-298	•	
		FLENEDR	21	299-305		
		FLENEDRR	22	299-306		
		SASLHLPK	23	307-314		
		LSITGTYDLK	24	315-324		
		SVLGQLGITK	25	325-334		
		VFSNGADLSGVTEEAPLK	26	335-352		
		AVLTIDEK	27	360-367		
4704	353	TDTSHHDQDHPTFNK	13	35-49	Alpha-1-antitrypsin	P01009
		FLEDVKK	15	154-160		
		KQINDYVEK	16	179-187		
		QINDYVEK	17	180-187		
		DTEEEDFHVDQATTVK (M1A allele)	18	226-241		
		DTEEEDFHVDQVTTVK (M1V allele)	61	226-241		
		LSSWVLLMK + 1 Oxidation (M)	28	259-267		
		FLENEDR	21	299-305		
		FLENEDRR	22	299-306		
		SASLHLPK	23	307-314		
		LSITGTYDLK	24	315-324		
		SVLGQLGITK	25	325-334		
		VFSNGADLSGVTEEAPLK	26	335-352		

Table 5. Identification of the protein spots that were altered between the studied groups.

exp2 AVLTIDEK 27 360-367 LGMFNIQHCK (Cys-CAM) 29 248-257 GINDYVEK 17 180-187 LSTGTYDLK 24 315-324 SVLGQLGITK 26 335-334 VFNGADLSGVTEEAPLK 26 335-332 LLELTGRK 30 86-93 FALVREDR 31 386-396 FALVREDR 32 313-320 BH LETPDFQLFK 34 32-41 ATWSGAVLAGR 36 26-53 LELTGPK 36 26-64 ATWSGAVLAGR 36 22-64 ATWSGAVLAGR 36 22-64 ATWSGAVLAGR 37 31-130 BH LETTOPPQLFK 36 22-64 VQPYLDDFQK 36 22-64 VQPYLDDFQK 37 121-130 B16.56f*ALKEDI360.25f* (aa 208: N → D) 38 201-212 AKPALEDLR 40 21-239 LLDNWDSVTSFFSK 44 48-64 LEALKENGGAR 45 202-212 QGLLPVLESFK	Spot	Spot	Peptide	Seq ID No.	aa	Identification in database	ID number
AVLTIDEK AVLTIDEK GMFNIQHCK (Cys-CAM) 355 QINDYVEK LGMFNIQHCK (Cys-CAM) 29 248-257 CABLOGLGTK SVLGQLGTK VFSNGADLSGVTEEAPLK 24 315-324 315-324 XVFSNGADLSGVTEEAPLK 26 335-352 LLELTGPK ATWSGAVLAGR 31 386-396 FALVREDR CLAPLEGAR (cys-CAM + ox) BH CLAPLEGAR (cys-CAM + ox) 31 386-396 LLETPDFQLFK ATWSGAVLAGR BH ATWSGAVLAGR S13 304-312 ATWSGAVLAGR BH ATWSGAVLAGR ATWSGAVLAGR 149 DYVSQFEGSALGK VQPYLDDFQK VQPYLDDFQK ATEHLSTLSEK ATEHLSTLSEK ATEHLSTLSEK ATEHLSTLSEK ATEHLSTLSEK ATEHLSTLSEK AKPALEDLR ATEHLSTLSEK ATEHLS	exp1	exp2					database
155 QINDYVEK 157 AGNEVIQHCK (Cys-CAM) 157 180-187 1580-1			AVLTIDEK	27	360-367		
355 QINDYVEK 17 180-187 LSITGTYDLK 24 315-324 SVLGQLGITK VFSNGADLSGVTEEAPLK 26 335-334 VFSNGADLSGVTEEAPLK 26 335-334 VFSNGADLSGVTEEAPLK 27 315-324 N6-93 LLELTGPK BH CLAPLEGAR (cys-CAM + ox) TAWSGAVLAGR BH ATWSGAVLAGR LETPDFQLFK ATWSGAVLAGR 13 386-396 LLELTGPK BH ATWSGAVLAGR 13 386-396 LLELTGPK ATWSGAVLAGR 13 386-396 LLELTGPK BH ATWSGAVLAGR 149 DYVSQFEGSALGK VQPYLDDFQK POLOSIAL ATSTACK POLOSIAL ATSTACK POLOSIAL ATSTACK POLOSIAL ATSTACK ATTALSTYNER ATTALSTYNER ATTALSTYNER BOSGRDYVSQFEGSALGK 44 48-64 LEALKENGGAR VORLPAEESR ANDONDSVTSTFSK BOSGRDYVSQFEGSALGK 47 143-155 COLLPVLESFR POLOSIAL ATSTACK POLOSIAL A			LGMFNIQHCK (Cys-CAM)	29	248-257		
LSITGTYDLK SVLGQLGTK SVLGQLGTK SVLGQLGTK SVLGQLGTK SYLGQLGTK SS-334 VFSNGADLSGVTEEAPLK LLELTGPK ATWSGAVLAGR 13 386-33 13 386-36 LLELTGRK ATWSGAVLAGR BH CLAPLEGAR (cys-CAM + ox) 13 304-312 14 CLAPLEGAR (cys-CAM + ox) EALVREDR ATWSGAVLAGR ATWSGAVLAGR LETTGPK LETTGPK LETTGPK LETTGPK LETTGPK ATWSGAVLAGR 149 DYVSQFEGSALGK VQPYLDDFQK ATEHLSTLSEK ATEHLSTLSEK ATEHLSTLSEK ATEHLSTLSEK AKPALEDLR LLDNWDSVTSTFSK BSGRDYVSQFEGSALGK ARPACE LLDNWDSVTSTFSK BSGRDYVSQFEGSALGK ARPACE LLDNWDSVTSTFSK AS 202-212 GGLLPVLESFK A 48-64 LEALKENGGAR VGPLAELOGAR A 48-64 LEALKENGGAR VGPLAELOGAR A 11-155 A 11-155	4705	355	QINDYVEK	17	180-187	Alpha-1-antitrypsin	P01009
SVLGQLGITK SVLGQLGITK VFSNGADLSGVTEEAPLK 26 335-352 LLELTGPK LLELTGPK 30 86-93 ATWSGAVLAGR FALVREDR 13 386-396 14 CLAPLEGAR (cys-CAM + ox) 13 304-312 FALVREDR LETPDFQLFK ATWSGAVLAGR 14 32-41 ATWSGAVLAGR 14 32-41 ATWSGAVLAGR LETTGPK 149 DYVSQFEGALGK VQPYLDDFQK PYLKEDI360.25]* (aa 208: N → D) 19 16.56]*ALKEDI360.25]* (aa 208: N → D) 19 16.56]*ALKEDI360.25]* ATEHLSTLSEK AKPALEDLR LDNWDSVTSTFSK AKPALEDLR LLDNWDSVTSTFSK BSGRDYVSQFEGSALGK 44 48-64 LEALKENGGAR VERTICEAR 149 1165-173 141-155 141-155	7206		LSITGTYDLK	24	315-324	Alpha-1-antitrypsin	P01009
RBH ULELTGPK LLELTGPK LLELTGPK 30 86-93 LLELTGPK ATWSGAVLAGR 4 CLAPLEGAR (cys-CAM + ox) 33 304-312 H ATWSGAVLAGR ATWSGAVLAGR BH ATWSGAVLAGR LLELTGPK ATWSGAVLAGR LLELTGPK BH ATWSGAVLAGR ATWSGAVLAGR 149 DYVSQFEGSALGK VQPYLDDFQK 149 DYVSQFEGSALGK ATEHLSTLSEK A			SVLGQLGITK	25	325-334	;	
RBH LLELTGPK 375 ATWSGAVLAGR 376.396 ATWSGAVLAGR 377.320 4 CLAPLEGAR (cys-CAM + ox) 577.313.320 4 SALVREDR BH CLETPDFQLFK ATWSGAVLAGR BH ATWSGAVLAGR LLELTGPK ATWSGAVLAGR 149 DYVSQFEGSALGK VQPYLDDFQK [916.56]*ALKED[360.25]* (aa 208 : N → D) ATHLSTLSEK AKPALEDLR LLENDWDSYTSTFSK DSGRDYVSQFEGSALGK ARPALEDLR LLENDWDSYTSTFSK DSGRDYVSQFEGSALGK ATHLAPYSDELR LLENUWDSYTSTFSK DSGRDYVSQFEGSALGK ATHLAPYSDELR LEALKENGGAR ATHLAPYSDELR LEALKENGGAR ATHLAPYSDELR LEALKENGGAR ATHLAPYSDELR LEALKENGGAR ATHLAPYSTER ATHLAPYSDELR			VFSNGADLSGVTEEAPLK	26	335-352		
375 ATWSGAVLAGR 31 386-396 FALVREDR CLAPLEGAR (cys-CAM + ox) 32 313-320 33 304-312 FALVREDR BH LETPDFQLFK 34 32-41 ATWSGAVLAGR LLELTGPK LLELTGPK 149 DYVSQFEGSALGK 36 52-64 VQPYLDDFQK [916.56] ⁺ ALKED[360.25] ⁺ (aa 208 : N → D) 38 201-212 ATEHLSTLSEK AKPALEDLR LLDNWDSVTSTFSK 149 DSGRDYVSQFEGSALGK 37 121-130 38 201-212 ATEHLSTLSEK AKPALEDLR LLDNWDSVTSTFSK 48-64 LEALKENGGAR CGLLPVLESFK 48-64 LEALKENGGAR AKPALEDLR LLDNWDSVTSTFSK AB-64 LEALKENGGAR AK-64-57 ATEHLSTLSEK AGLEDLR AKPALEDLR AKPALEDL	4801RBH		LLELTGPK	30	86-93	Alpha-1B-glycoprotein	P04217
H CLAPLEGAR (cys-CAM + ox) CLAPLEGAR (cys-CAM + ox) FALVREDR BH LETPDFQLFK ATWSGAVLAGR LLELTGPK EVPLNTIFMGR + 1 Oxidation (M) BY OQPYLDDFQK ATEHLSTLSEK ATEHLSTLSEK AKPALEDLR LSPLGEEMR + 1 Oxidation (M) 165-173 THLAPYSDELR LEALKENGGAR AKPALEDLR LSPLGEEMR + 1 Oxidation (M) LSPLGEEMR + 1 Oxidation (M) LSPLGEEMR + 1 Oxidation (M) ATEHLSTLSEK ACTORIAN AND AND AND AND AND AND AND	4803	375	ATWSGAVLAGR	31	386-396	Alpha-1B-glycoprotein	P04217
H CLAPLEGAR (cys-CAM + ox) 33 304-312 FALVREDR LETPDFQLFK ATWSGAVLAGR LETPDFQLFK ATWSGALAGR LETPDFQLFK ATWSGALAGR 149 DYVSQFEGSALGK VQPYLDDFQK [916.56]*ALKED[360.25]* (aa 208 : N → D) 38 201-212 ATEHLSTLSEK AKPALEDLR LSPLGEMR + 1 Oxidation (M) 41 165-173 THLAPYSDELR LLDNWDSVTSTFSK DSGRDYVSQFEGSALGK 44 48-64 LEALKENGGAR VEPLRAELQEGAR VEPLRAELQEGAR 149 165-173 THLAPYSDELR LEALKENGGAR VEPLRAELQEGAR 141 165-173 THLAPYSDELR LEALKENGGAR VEPLRAELQEGAR VEPLRAE			FALVREDR	32	313-320		
ETALVREDR BH LETPDFQLFK ATWSGAVLAGR LLELTGPK 149 DYVSQFEGSALGK 149 DYVSQFEGSALGK 149 DYVSQFEGSALGK 140 DYVSQFEGSALGK 140 DYVSQFEGSALGK 140 DYVSQFEGSALGK 140 DYVSQFEGSALGK 140 140 140 140 140 151-130 1616.56]⁺ALKED[360.25]⁺ (aa 208 : N → D) 17 171-130 18 201-212 ATEHLSTLSEK AKPALEDLR ATEHLSTLSEK ATEHLSTLSEK ATEHLSTSEK ATEHCSTSEK	IRBH		CLAPLEGAR (cys-CAM + ox)	33	304-312	Alpha-1B-glycoprotein	P04217
BH LETPDFQLFK ATWSGAVLAGR ATWSGAVLAGR LLELTGPK LLELTGPK EVPLNTIIFMGR + 1 Oxidation (M) 149 DYVSQFEGSALGK VQPYLDDFQK [916.56] ⁺ ALKED[360.25] ⁺ (aa 208 : N → D) ATEHLSTLSEK ATEHLSTLSEK AKPALEDLR LSPLGEEMR + 1 Oxidation (M) ATHAPYSDELR LEALKENGGAR ATHAPYSDELR COCLIPYLESFK ATHAPYSDELR ATHAPYSD			FALVREDR	32	313-320		
ATWSGAVLAGR LLELTGPK LLELTGPK 30 86-93 EVPLNTIIFMGR + 1 Oxidation (M) 149 DYVSQFEGSALGK VQPYLDDFQK [916.56]*ALKED[360.25]* (aa 208 : N → D) ATEHLSTLSEK ATEHLSTLSEK AKPALEDLR LSPLGEEMR + 1 Oxidation (M) 140 151-130 37 121-130 39 220-230 AKPALEDLR LSPLGEEMR + 1 Oxidation (M) 165-173 THLAPYSDELR LLDNWDSVTSTFSK DSGRDYVSQFEGSALGK 44 48-64 LEALKENGGAR QGLLPVLESFK VEPLRAELQEGAR 47 143-155	901RBH		LETPDFQLFK	34	32-41	Alpha-1B-glycoprotein	P04217
LLELTGPK EVPLNTIIFMGR + 1 Oxidation (M) 35 446-457 149 DYVSQFEGSALGK VQPYLDDFQK [916.56]*ALKED[360.25]* (aa 208 : N → D) 38 201-212 ATEHLSTLSEK AKPALEDLR LSPLGEEMR + 1 Oxidation (M) 41 165-173 THLAPYSDELR LLDNWDSVTSTFSK DSGRDYVSQFEGSALGK LEALKENGGAR VEPLRAELQEGAR VEPLRAELQEGAR VEPLRAELQEGAR 149 86-93 446-457 447-155			ATWSGAVLAGR	31	386-396		
EVPLNTIIFMGR + 1 Oxidation (M) 35 446-457 149 DYVSQFEGSALGK VQPYLDDFQK [916.56] ⁺ ALKED[360.25] ⁺ (aa 208 : N → D) 38 201-212 ATEHLSTLSEK AKPALEDLR LSPLGEEMR + 1 Oxidation (M) 41 165-173 THLAPYSDELR LLDNWDSVTSTFSK DSGRDYVSQFEGSALGK LEALKENGGAR QGLLPVLESFK VEPLRAELQEGAR 143-155 VEPLRAELQEGAR			LLELTGPK	30	86-93		
149 DYVSQFEGSALGK VQPYLDDFQK (916.56] ⁺ ALKED[360.25] ⁺ (aa 208 : N → D) ATEHLSTLSEK ATEHLSTLSEK AKPALEDLR LSPLGEEMR + 1 Oxidation (M) LSPLGEEMR + 1 Oxidation (M) THLAPYSDELR LLDNWDSVTSTFSK DSGRDYVSQFEGSALGK LEALKENGGAR CGLLPVLESFK VEPLRAELQEGAR 143 70-83 QGLLPVLESFK VEPLRAELQEGAR 47 143-155	5702	-	_	35	446-457	Antithrombin-III	P01008
VQPYLDDFQK 37 121-130 [916.56]*ALKED[360.25]* (aa 208 : N \rightarrow D) 38 201-212 ATEHLSTLSEK 39 220-230 AKPALEDLR 40 231-239 LSPLGEEMR + 1 Oxidation (M) 41 165-173 THLAPYSDELR 42 185-195 LLDNWDSVTSTFSK 43 70-83 DSGRDYVSQFEGSALGK 44 48-64 LEALKENGGAR 45 202-212 QGLLPVLESFK 46 240-250 VEPLRAELQEGAR 47 143-155	6102	149		36	52-64	Apolipoprotein A-I	P02647
[916.56] ⁺ ALKED[360.25] ⁺ (aa 208 : N → D) 38 201-212 ATEHLSTLSEK AKPALEDLR 40 231-239 LSPLGEEMR + 1 Oxidation (M) 41 165-173 THLAPYSDELR LLDNWDSVTSTFSK DSGRDYVSQFEGSALGK LEALKENGGAR QGLLPVLESFK VEPLRAELQEGAR 143 70-83 202-212 QGLLPVLESFK 46 240-250			VQPYLDDFQK	37	121-130		
ATEHLSTLSEK AKPALEDLR AKPALEDLR LSPLGEEMR + 1 Oxidation (M) THLAPYSDELR LLDNWDSVTSTFSK DSGRDYVSQFEGSALGK LEALKENGGAR QGLLPVLESFK VEPLRAELQEGAR 143-155			$[916.56]^{+}$ ALKED $[360.25]^{+}$ (aa 208 : N \rightarrow D)	38	201-212		
AKPALEDLR LSPLGEEMR + 1 Oxidation (M) 41 165-173 THLAPYSDELR LLDNWDSVTSTFSK 43 70-83 DSGRDYVSQFEGSALGK 44 48-64 LEALKENGGAR 45 202-212 QGLLPVLESFK 46 240-250 VEPLRAELQEGAR 47 143-155			ATEHLSTLSEK	39	220-230		
LSPLGEEMR + 1 Oxidation (M) THLAPYSDELR LLDNWDSVTSTFSK 43 70-83 DSGRDYVSQFEGSALGK 44 48-64 LEALKENGGAR QGLLPVLESFK VEPLRAELQEGAR 47 143-155			AKPALEDLR	40	231-239		
THLAPYSDELR LLDNWDSVTSTFSK 43 70-83 LLDNWDSVTSTFSK 44 48-64 LEALKENGGAR QGLLPVLESFK VEPLRAELQEGAR 45 202-212 46 240-250			LSPLGEEMR + 1 Oxidation (M)	41	165-173		
LLDNWDSVTSTFSK DSGRDYVSQFEGSALGK 44 48-64 LEALKENGGAR QGLLPVLESFK VEPLRAELQEGAR 47 143-155			THLAPYSDELR	42	185-195		
DSGRDYVSQFEGSALGK LEALKENGGAR 44 48-64 45 202-212 QGLLPVLESFK 46 240-250 VEPLRAELQEGAR 47 143-155			LLDNWDSVTSTFSK	43	70-83		
LEALKENGGAR QGLLPVLESFK VEPLRAELQEGAR 45 202-212 46 240-250			DSGRDYVSQFEGSALGK	44	48-64		
QGLLPVLESFK 46 240-250 VEPLRAELQEGAR 47 143-155			LEALKENGGAR	45	202-212		
VEPLRAELQEGAR 47 143-155			QGLLPVLESFK	46	240-250		
17 C			VEPLRAELQEGAR	47	143-155		
146 DYVSQFEGSALGK 36 52-64	6303	146	DYVSQFEGSALGK	36	52-64	Apolipoprotein A-I	P02647

Table 5. Identification of the protein spots that were altered between the studied groups.

exp1 exp2	,		1		
		ı			database
	VQPYLDDFQK	37	121-130		
	$[916.56]^{+}$ ALKED $[360.27]^{+}$ (aa208: N \rightarrow D)	38	201-212		
	ATEHLSTLSEK	39	220-230		
	LSPLGEEMRDR + 1 Oxidation (M)	48	165-175		
	LSPLGEEMR + 1 Oxidation (M)	41	165-173		
	THLAPYSDELR	42	185-195		
7101 285	DSGRDYVSQFEGSALGK	44	48-64	Apolipoprotein A-I	P02647
	DYVSQFEGSALGK	36	52-64		
	[1315.83] [†] DNDDSVTSTFSK (aa 74: W→D)	49	70-83		
	QEMSKDLEEVK + 1 Oxidation (M)	20	108-118		
		37	121-130		
	VQPYLDDFQKK	51	121-131		
	LSPLGEEMR + 1 Oxidation (M)	41	165-173		
	LSPLGEEMRDR + 1 Oxidation (M)	48	165-175		
	THLAPYSDELR	42	185-195		
	LEALKED[360.25] ⁺ (aa 208 : N \rightarrow D)	52	202-212		
	LEALKENGGAR	45	202-212		
	ATEHLSTLSEK	39	220-230		
	AKPALEDLR	40	231-239		
	DLATVYVDVLK	53	237-247		
	QGLLPVLESFK	46	240-250		
	QKLHELQEK (E → pyroglutamic acid)	54	156-164		
	VEPLRAELQEGAR	47	143-155		
	LLDNWDSVTSTFSK	43	70-83		
	DEPPQSPWDR + 1 Oxidation (W)	55	25-34		
	DLATVYVDVLK	53	37-47		
	VSFLSALEEYTK	95	251-262		
	KWQEEMELYR + 1 Oxydation (M)	57	131-140		

Table 5. Identification of the protein spots that were altered between the studied groups.

Spot	Spot	Peptide	Seq ID No.	aa	Identification in database	ID number
exp1	exp2					database
4310	144	THLAPYSDELR	42	185-195	Apolipoprotein A-I	P02647
	143	THLAPYSDELR	42	185-195	Apolipoprotein A-I	P02647
4606+4605		LGEVNTYAGDLQK	58	82-99	Apolipoprotein A-IV	P06727
		LLPHANEVSQK	59	113-123	,	
		QLTPYAQR	09	156-163		
		IDQNVEELKGR	61	190-200		
		LTPYADEFK	62	201-209		
		ISASAEELR	63	256-264		
		LAPLAEDVR	64	267-275		
		ALVQQMEQLR + 1 Oxidation (M)	65	317-326		
5402	81	LEPYADQLR	99	135-143	Apolipoprotein A-IV	P06727
		IDQNVEELKGR	<u>6</u> 1	190-200		
		LTPYADEFK	62	201-209		
		IDQTVEELR	<i>L</i> 9	212-220		
		ISASAEELR	63	257-264		
		LAPLAEDVR	64	267-275		
		ALVQQMEQLR + 1 Oxidation (M)	65	317-326		
		RVEPYGENFNK	89	306-317		
		SLAPYAQDTQEK	69	222-233		
		LGEVNTYAGDLQK	28	82-99		
6502		KVEQAVETEPEPELR	4	19-33	Apolipoprotein E	P02649
		AYKSELEEQLTPVAEETR	11	91-109	•	
		LSKELQAAQAR	12	111-121		
		AATVGSLAGQPLQER	7	210-224		
		AKLEEQAQQIR	2	259-269		
		LQAEAFQAR	1	270-278		
5502	110	LQAEAFQAR	-	270-278	Apolipoprotein E	P02649
		AKLEEQAQQIR	2	259-269		

Table 5. Identification of the protein spots that were altered between the studied groups.

Spot	Spot	Peptide	Seq ID No.	22	Identification in database	ID number
expl	exp2					database
		LLRDADDLQK	3	166-175		
		KVEQAVETEPEPELR	4	19-33		
	114	LQAEAFQAR		270-278	Apolipoprotein E	P02649
		AKLEEQAQQIR	2	259-269		
		LGPLVEQGR	Ş	199-207		
		VQAAVGTSAAPVPSDNH	9	301-317		
	272	LGPLVEQGR	5	199-207	Apolipoprotein E	P02649
	862	LGPLVEQGR	5	199-207	Apolipoprotein E	P02649
	681	KVEQAVETEPEPELR	4	19-33	Apolipoprotein E	P02649
	480	LQAEAFQAR	-	270-278	Apolipoprotein E	P02649
		LGPLVEQGR	5	199-207		
		AKLEEQAQQIR	2	259-269		
		ALMDETMKELK + 2 Oxidations (M)	70	06-08		
3405		ELDESLQVAER	71	326-336	Apolipoprotein J	P10909
3505		ELDESLQVAER	71	326-336	Apolipoprotein J	P10909
4401	323	ELDESLQVAER	71	326-336	Apolipoprotein J	P10909
		KYNELLK	72	340-346		
		FMETVAEK + 1 Oxidation (M)	73	430-437		
5302	108	ELDESLQVAER	71	326-336	Apolipoprotein J	P10909
		EILSVDCSTNNPSQAK + 1 (cys-CAM)	74	307-322		
8601		TLLSNLEEAK	75	82-69	Apolipoprotein J	P10909
		IDSLLENDR	9/	159-167		
		ASSIIDELFQDR	77	183-194		
5202		AGALNSNDAFVLK	78	585-597	Gelsolin	P06396
		YIETDPANR	79	730-738		
6404		AGALNSNDAFVLK	78	585-597	Gelsolin	P06396
		TGAQELLR	80	616-623		
5004	411	TEGDGVYTLNDKK	81	60-72	Haptoglobin-1/2	P00737

Table 5. Identification of the protein spots that were altered between the studied groups.

	spor exp2	repliae	Seq ID No.	e e	Identification in database	ID number database
				119-131		P00738
		TEGDGVYTLNDKKQWINK + 1 ox (W)	82	<i>21-</i> 09		P00737
			٠	119-136		P00738
5903RBH		NFPSPVDAAFR	83	92-102	Hemopexin	P02790
		GGYTLVSGYPK	84	333-343		
8902RBH		NFPSPVDAAFR	83	92-102	Hemopexin	P02790
		QGHNSVFLIK	85	103-112		
		DYFMPCPGR + 1 (cys-CAM + ox) + 1	98	226-234		
		0x (M)				
		GGYTLVSGYPK	84	333-343		
4701RBH		SAVQGPPER	87	169-177	Ig alpha-1 chain C region	P01876
					(heavy)	
		QEPSQGTTTFAVTSILR	88	283-299		
4804		TPLTATLSK	68	213-221	Ig alpha-1 chain C region	P01876
					(heavy)	
4702		TVGSDTFYSFK	06	65-75	Kininogen	P01042
		QVVAGLNFR	91	188-196		
		YFIDFVAR	92	317-324		
8101		APEAQVSVQPNFQQDK	93	23-38	Prostaglandin-H2 D-	P41222
					isomerase	
		TMLLQPAGSLGSYSYR + 1 Oxidation (M)	94	93-108		
		AQGFTEDTIVFLPQTDK	95	169-185		
6026		[1617.85]*EAQVSVQPNF[518.26]*	96	23-38	Prostaglandin-H2 D-	P41222
					isomerase	
		TMLLQPAGSLGSYSYR + 1 Oxidation (M)	94	93-108		
6001		AADDTDEPFASGK (aa 61 : W \rightarrow D)	24	89-95	Transthyretin	P02766
7102		[603.41]PLMVK	86	21-35	Transthyretin	P02766
7108	274	GPTGTGESKCPLMVK (Cys(O ₃ H))	66	21-35	Transthyretin	P02766

Table 5. Identification of the protein spots that were altered between the studied groups.

Spot exp1	Spot exn2	Peptide	Seq ID No.	aa	Identification in database	D number database
		GPTGTGESKCPLMVK (Cys(O ₃ H)/ M:	66	21-35		
		AADDTWEPFASGK (W + 2*16 Da)	100	26-68		
		AADDTDEPFASGK (aa 61 : W \rightarrow D)	76	89-95		
		AADDTWEPFASGK	100	99-95		
		KAADDTWEPFASGK	102	55-68		
		TSESGELHGLTTEEEFVEGIYK	103	06-69		
3601RBH		HLSLLTTLSNR	104	208-218	Vitamin D-binding protein	P02774
		YTFELSR	105	346-352		
		THLPEVFLSK	106	354-363		
		VLEPTLK	107	364-370		
		ELSSFIDK	108	395-402		
4411		VCSQYAAYGEK (cys-CAM + ox)	109	219-229	Vitamin D-binding protein	P02774
		VMDKYTFELSR + 1 Oxidation (M)	110	342-352	ř	
		YTFELSR	105	346-352		
		THLPEVFLSK	106	354-363		
		VLEPTLK	107	364-370		
		[1433.61] CCDVEDSTTCFNAK (1 cys-CAM	111	371-388		
		+ ox, 2 Dha)				
		ELSSFIDK	108	395-402		
		AKLPDATPK	112	428-436		
2402	8	AGEVQEPELR	113	239-248	Zinc-alpha-2-glycoprotein	P25311
		QDPPSVVVTSHQAPGEK	101	201-217		